



22000-20603.10-Seq

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun
Ishihari, Hiroaki
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease Activated Receptor
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- E1 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Catherine M. Polizzi
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 22000-20604.00
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 813-5600
(B) TELEFAX: (650) 494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGA CTTTGTA TACTTAACAA CATCCTGTAG CCGGGTCTCA GGACATCAAG ATGAAAATCC
 60
 TTATCTTGGT TGCAGCTGGG CTGCTGTTTC TGCCAGTCAC TGTTTGCCAA AGTGGCATAA
 120
 ATGTTTCAGA CAACTCAGCA AAGCCAACCT TAACTATTAA GAGTTTTAAT GGGGGTCCCC
 180
 AAAATACCTT TGAAGAATTC CCACTTTCTG ACATAGAGGG CTGGACAGGA GCCACCACAA
 240
 CTATAAAAGC GGAGTGTCCC GAGGACAGTA TTTCAACTCT CCACGTGAAT AATGCTACCA
 300
 TAGGATACCT GAGAAGTTCC TTAAGTACCC AAGTGATACC TGCCATCTAT ATCCTGCTGT
 360
 TTGTGGTTGG TGTACCATCC AACATCGTGA CCCTGTGGAA ACTCTCCTTA AGGACCAAAT
 420
 CCATCAGTCT GGTCATCTTT CACACCAACC TGGCCATCGC AGATCTCCTT TTCTGTGTCA
 480
 CACTGCCATT TAAGATCGCC TACCATCTCA ATGGCAACAA CTGGGTATTT GGCGAGGTCA
 540
 TGTGCCGGAT CACCACGGTC GTTTTCTACG GCAACATGTA CTGCGCTATC CTGATCCTCA
 600
 CTTGCATGGG CATCAACCGC TACCTGGCCA CGGCTCACCC TTTCACATAC CAGAAGCTGC
 660
 CCAAACGCAG CTTCTCCTTG CTCATGTGTG GCATAGTGTG GGTCATGGTT TTCTTATACA
 720
 TGCTGCCCTT TGTCATCCTG AAGCAGGAGT ACCACCTCGT CCACTCAGAG ATCACCACCT
 780
 GCCACGATGT CGTCGACGCG TGCGAGTCCC CATCATCCTT CCGATTCTAC TACTTCGTCT
 840
 CCTTAGCATT CTTTGGGTTC CTCATCCCGT TTGTGATCAT CATCTTCTGT TACACGACTC
 900
 TCATCCACAA ACTTAAATCA AAGGATCGGA TATGGCTGGG CTACATCAAG GCCGTCCTCC
 960
 TCATCCTTGT GATTTTCACA ATTTGCTTTG CCCCCACCA CATCATACTC GTAATCCACC 1
 020
 ATGCCAACTA CTACTACCAC AATACCGACA GCTTGTACTT TATGTATCTT ATTGCTCTGT 1
 080

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GCCTGGGGAG CCTGAATAGC TGCCTAGATC CATTCCTTTA CTTTGTTCATG TCGAAAGTTG 1
140
TAGATCAGCT TAATCCTTAG TCGGCAATGG CAAGACCACT TTAGAGACCA AGGAGAGATA 1
200
TCTGGGAAGA CATACTGCT TGGC 1
224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA ATATTTCTT TCAATTACAG GCATAAATGT TTCAGACAAC TCAGCAAAGC
60
CAACCTTAAC TATTAAGAGT TTTAATGGGG GTCCCCAAAA TACCTTTGAA GAATTCNNNN
120
NNNTACAACT CTCCATGTGA ATAATGCTAC CATGGGATAC CTGAGAAGTT CCTTAAGTAC
180
CAAAGTGATA CCTGCCATCT ACATCCTGGT GTTTGTGATT GGTGTACCAG CGAACATCGT
240
GACCCTGTGG AACTCTCCT CAAGGACCAA ATCCATCTGT CTGGTCATCT TTCACACCAA
300
CCTGGCCATC GCGGATCTCC TTTTCTGTGT CACGCTGCCG TTTAAGATCN NCCTACCATC
360
TCAATGGCAA CAACTGGGTA TTTGGCGAGG TCATGTGCCG GATCACCACG GTCGTTTTCT
420
ACGGCAACAT GTACTGCGCT ANNNTCCTGA TCCTCACCTG CATGGGCATC AACCGCTACC
480
TGGCCACGGC TCACCCTTTC ACATACCAGA AGCTGCCCAA ACGCAGCTTC TCCATGCTCA
540
TGTGTGGCAT GGTGTGGGTC ATGGTTTTCT TATACATGCT GCCCTTTGTC ATCCNNNAAG
600
CAGGAGTACC ACCTCGTCCA CTCCGAGATC ACCACCTGCC ACGATGTCGT CGACGCGTGC
660
GANTCCCCAT CATCCTTCCG ATTCTACTAC TTCGTCTCCT TAGCATTCTT TGGGTTCCTC
720
ATCCCGTTTG TGATCATCAT CTTCTGTTAC ACGACTCTCA TCCACAACT TAAATCAAAA
780
GATCNGATAT GGCTGGGCTA CATCAAGGCC GTCCTCCTCA TCCTTGTGAA TTTCACCATC
840

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TGCTTCCCCC CCACCAAGNN NNNNGATATC TGGGAAGACG TACATGCTTG GCTGACTTGT
 900
 GCATGGCACC ATCAGCTCAA TTTTAAATTT TTTAATTTTA ATTTAATTTA ATTTTATGTT
 960
 TTTGAGACAG AGCCTCACTG TGTAGTCCTG GCTGGCCTGG CTGGTTCTCT ATTTAGACCA 1
 020
 GGTTAGCCTT GAACTCACAG AGATCTGCCT GCTTCTGCCT CCCAAGTGCT GGGTTCAACC 1
 080
 AGGTCTGGCA AGCGCTCCAT TTTTCAGCTC CTCTGCAACA GTGC 1
 124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu Tyr Thr Xaa Gln His Pro Val Ala Gly Ser Gln Asp Ile Lys
 1 5 10 15
 Met Lys Ile Leu Ile Leu Val Ala Ala Gly Leu Leu Phe Leu Pro Val
 20 25 30
 Thr Val Cys Gln Ser Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro
 35 40 45
 Thr Leu Thr Ile Lys Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu
 50 55 60
 Glu Phe Pro Leu Ser Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr
 65 70 75 80
 Ile Lys Ala Glu Cys Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn
 85 90 95
 Asn Ala Thr Ile Gly Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile
 100 105 110
 Pro Ala Ile Tyr Ile Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile
 115 120 125
 Val Thr Leu Trp Lys Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val
 130 135 140
 Ile Phe His Thr Asn Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr
 145 150 155 160
 Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe

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				165					170					175			
Gly	Glu	Val	Met	Cys	Arg	Ile	Thr	Thr	Val	Val	Phe	Tyr	Gly	Asn	Met		
			180						185				190				
Tyr	Cys	Ala	Ile	Leu	Ile	Leu	Thr	Cys	Met	Gly	Ile	Asn	Arg	Tyr	Leu		
		195					200					205					
Ala	Thr	Ala	His	Pro	Phe	Thr	Tyr	Gln	Lys	Leu	Pro	Lys	Arg	Ser	Phe		
	210					215					220						
Ser	Leu	Leu	Met	Cys	Gly	Ile	Val	Trp	Val	Met	Val	Phe	Leu	Tyr	Met		
225					230					235					240		
Leu	Pro	Phe	Val	Ile	Leu	Lys	Gln	Glu	Tyr	His	Leu	Val	His	Ser	Glu		
			245						250					255			
Ile	Thr	Thr	Cys	His	Asp	Val	Val	Asp	Ala	Cys	Glu	Ser	Pro	Ser	Ser		
			260					265					270				
Phe	Arg	Phe	Tyr	Tyr	Phe	Val	Ser	Leu	Ala	Phe	Phe	Gly	Phe	Leu	Ile		
	275						280					285					
Pro	Phe	Val	Ile	Ile	Ile	Phe	Cys	Tyr	Thr	Thr	Leu	Ile	His	Lys	Leu		
	290					295					300						
Lys	Ser	Lys	Asp	Arg	Ile	Trp	Leu	Gly	Tyr	Ile	Lys	Ala	Val	Leu	Leu		
305					310					315					320		
Ile	Leu	Val	Ile	Phe	Thr	Ile	Cys	Phe	Ala	Pro	Thr	Asn	Ile	Ile	Leu		
			325					330					335				
Val	Ile	His	His	Ala	Asn	Tyr	Tyr	Tyr	His	Asn	Thr	Asp	Ser	Leu	Tyr		
			340					345					350				
Phe	Met	Tyr	Leu	Ile	Ala	Leu	Cys	Leu	Gly	Ser	Leu	Asn	Ser	Cys	Leu		
	355						360					365					
Asp	Pro	Phe	Leu	Tyr	Phe	Val	Met	Ser	Lys	Val	Val	Asp	Gln	Leu	Asn		
	370					375						380					
Pro	Xaa	Ser	Ala	Met	Ala	Arg	Pro	Leu	Xaa	Arg	Pro	Arg	Arg	Asp	Ile		
385					390					395					400		
Trp	Glu	Asp	Ile	His	Ala	Trp											
				405													

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCTCCATGA TTTTACAGAT TTCATAACGT TTAAGAGACG GGA CTCAGGT CATCAAAATG
60
AAAGCCCTCA TCTTTGCAGC TGCTGGCCTC CTGCTTCTGT TGCCCACTTT TTGTCAGAGT
120

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GGCATGGAAA ATGATACAAA CAACTTGGCA AAGCCAACCT TACCCATTAA GACCTTTCGT
180
GGAGCTCCCC CAAATTCTTT TGAAGAGTTC CCCTTTTCTG CCTTGGAAGG CTGGACAGGA
240
GCCACGATTA CTGTAAAAAT TAAGTGCCCT GAAGAAAGTG CTTACATCT CCATGTGAAA
300
AATGCTACCA TGGGGTACCT GACCAGCTCC TTAAGTACTA AACTGATACC TGCCATCTAC
360
CTCCTGGTGT TTGTAGTTGG TGTCCCGGCC AATGCTGTGA CCCTGTGGAT GCTTTTCTTC
420
AGGACCAGAT CCATCTGTAC CACTGTATTC TACACCAACC TGGCCATTGC AGATTTTCTT
480
TTTTGTGTTA CATTGCCCTT TAAGATAGCT TATCATCTCA ATGGGAACAA CTGGGTATTT
540
GGAGAGGTCC TGTGCCGGGC CACCACAGTC ATCTTCTATG GCAACATGTA CTGCTCCATT
600
CTGCTCCTTG CCTGCATCAG CATCAACCGC TACCTGGCCA TCGTCCATCC TTTCACCTAC
660
CGGGGCCTGC CCAAGCACAC CTATGCCTTG GTAACATGTG GACTGGTGTG GGCAACAGTT
720
TTCTTATATA TGCTGCCATT TTTCATACTG AAGCAGGAAT ATTATCTTGT TCAGCCAGAC
780
ATCACCACCT GCCATGATGT TCACAACACT TGCAGATCCT CATCTCCCTT CCAACTCTAT
840
TACTTCATCT CTTTGGCATT CTTTGGATTC TTAATTCCAT TTGTGCTTAT CATCTACTGC
900
TATGCAGCCA TCATCCGGAC ACTTAATGCA TACGATCATA GATGGTTGTG GTATGTTAAG
960
GCGAGTCTCC TCATCCTTGT GATTTTTTACC ATTTGCTTTG CTCCAAGCAA TATTATTCTT 1
020
ATTATTCACC ATGCTAACTA CTACTIONAAC AACACTGATG GCTTATATTT TATATATCTC 1
080
ATAGCTTTGT GCCTGGGTAG TCTTAATAGT TGCTTAGATC CATTCCCTTA TTTTCTCATG 1
140
TCAAAAACCA GAAATCACTC CACTGCTTAC CTTACAAAAT AGTGAAATGA TCTTAGAGAA 1
200
CAAGGACAGC CATCACAGAG AACG 1
224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG AAAATGATAC AAACAACCTTG GCAAAGCCAA CCTTACCCAT TAAGACCTTT
60
CGTGGAGCTC CCCCAAATTC TTTTGAAGAG TTCCCCTTTT CTGCCTTGGA AGGCTGGACA
120
GGAGCCACGA TTA CTGTAAA AATTAAGTGC CCTGAAGAAA GTGCTTCACA TCTCCATGTG
180
AAAAATGCTA CCATGGGGTA CCTGACCAGC TCCTTAAGTA CTAAACTGAT ACCTGCCATC
240
TACCTCCTGG TGTTTGTAGT TGGTGTCCCG GCCAATGCTG TGACCCTGTG GATGCTTTTC
300
TTCAGGACCA GATCCATCTG TACCACTGTA TTCTACACCA ACCTGGCCAT TGCAGATTTT
360
CTTTTTTGTG TTACATTGCC CTTTAAGATA GCTTATCATC TCAATGGGAA CAACTGGGTA
420
TTTGGAGAGG TCCTGTGCCG GGCCACCACA GTCATCTTCT ATGGCAACAT GTACTGCTCC
480
ATTCTGCTCC TTGCCTGCAT CAGCATCAAC CGCTACCTGG CCATCGTCCA TCCTTTCACC
540
TACCGGGGCC TGCCCAAGCA CACCTATGCC TTGGTAACAT GTGGACTGGT GTGGGCAACA
600
GTTTTCTTAT ATATGCTGCC ATTTTTCATA CTGAAGCAGG AATATTATCT TGTTTCAGCCA
660
GACATCACCA CCTGCCATGA TGTTCAACAAC ACTTGCGAGT CCTCATCTCC CTTCCAACCTC
720
TATTA CTTC TCTCCTTGGC ATTCTTTGGA TTCTTAATTC CATTTGTGCT TATCATCTAC
780
TGCTATGCAG CCATCATCCG GACACTTAAT GCATACGATC ATAGATGGTT GTGGTATGTT
840
AAGGCGAGTC TCCTCATCCT TGTGATTTTT ACCATTTGCT TTGCTCCAAG CAATATTATT
900
CTTATTATTC ACCATGCTAA CTACTACTAC AACAACACTG ATGGCTTATA TTTTATATAT
960
CTCATAGCTT TGTGCCTGGG TAGTCTTAAT AGTTGCTTAG ATCCATTCCT TTATTTTCTC 1
020
ATGTCAAAAA CCAGAAATCA CTCCACTGCT TACCTTACAA AATAGTGAAA TGATCTTAGA 1
080
GAACAAGGAC AGCCATCACA GA 1
102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 9, 394, 395

(D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Ser	Met	Ile	Leu	Gln	Ile	Ser	Xaa	Arg	Leu	Arg	Asp	Gly	Thr	Gln
1				5				10						15	
Val	Ile	Lys	Met	Lys	Ala	Leu	Ile	Phe	Ala	Ala	Ala	Gly	Leu	Leu	Leu
			20					25					30		
Leu	Leu	Pro	Thr	Phe	Cys	Gln	Ser	Gly	Met	Glu	Asn	Asp	Thr	Asn	Asn
		35					40					45			
Leu	Ala	Lys	Pro	Thr	Leu	Pro	Ile	Lys	Thr	Phe	Arg	Gly	Ala	Pro	Pro
	50					55					60				
Asn	Ser	Phe	Glu	Glu	Phe	Pro	Phe	Ser	Ala	Leu	Glu	Gly	Trp	Thr	Gly
65					70					75					80
Ala	Thr	Ile	Thr	Val	Lys	Ile	Lys	Cys	Pro	Glu	Glu	Ser	Ala	Ser	His
				85					90					95	
Leu	His	Val	Lys	Asn	Ala	Thr	Met	Gly	Tyr	Leu	Thr	Ser	Ser	Leu	Ser
			100					105					110		
Thr	Lys	Leu	Ile	Pro	Ala	Ile	Tyr	Leu	Leu	Val	Phe	Val	Val	Gly	Val
	115						120						125		
Pro	Ala	Asn	Ala	Val	Thr	Leu	Trp	Met	Leu	Phe	Phe	Arg	Thr	Arg	Ser
	130					135						140			
Ile	Cys	Thr	Thr	Val	Phe	Tyr	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Phe	Leu
145					150					155					160
Phe	Cys	Val	Thr	Leu	Pro	Phe	Lys	Ile	Ala	Tyr	His	Leu	Asn	Gly	Asn
				165					170					175	
Asn	Trp	Val	Phe	Gly	Glu	Val	Leu	Cys	Arg	Ala	Thr	Thr	Val	Ile	Phe
		180						185					190		
Tyr	Gly	Asn	Met	Tyr	Cys	Ser	Ile	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Ile
	195					200						205			
Asn	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Phe	Thr	Tyr	Arg	Gly	Leu	Pro
	210					215					220				
Lys	His	Thr	Tyr	Ala	Leu	Val	Thr	Cys	Gly	Leu	Val	Trp	Ala	Thr	Val
225					230					235					240
Phe	Leu	Tyr	Met	Leu	Pro	Phe	Phe	Ile	Leu	Lys	Gln	Glu	Tyr	Tyr	Leu
				245					250					255	
Val	Gln	Pro	Asp	Ile	Thr	Thr	Cys	His	Asp	Val	His	Asn	Thr	Cys	Glu
			260					265					270		
Ser	Ser	Ser	Pro	Phe	Gln	Leu	Tyr	Tyr	Phe	Ile	Ser	Leu	Ala	Phe	Phe
		275					280					285			
Gly	Phe	Leu	Ile	Pro	Phe	Val	Leu	Ile	Ile	Tyr	Cys	Tyr	Ala	Ala	Ile
	290					295					300				
Ile	Arg	Thr	Leu	Asn	Ala	Tyr	Asp	His	Arg	Trp	Leu	Trp	Tyr	Val	Lys

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305		310		315		320									
Ala	Ser	Leu	Leu	Ile	Leu	Val	Ile	Phe	Thr	Ile	Cys	Phe	Ala	Pro	Ser
		325					330							335	
Asn	Ile	Ile	Leu	Ile	Ile	His	His	Ala	Asn	Tyr	Tyr	Tyr	Asn	Asn	Thr
		340						345					350		
Asp	Gly	Leu	Tyr	Phe	Ile	Tyr	Leu	Ile	Ala	Leu	Cys	Leu	Gly	Ser	Leu
		355					360					365			
Asn	Ser	Cys	Leu	Asp	Pro	Phe	Leu	Tyr	Phe	Leu	Met	Ser	Lys	Thr	Arg
		370				375					380				
Asn	His	Ser	Thr	Ala	Tyr	Leu	Thr	Lys	Xaa	Xaa	Asn	Asp	Leu	Arg	Glu
385					390				395						400
Gln	Gly	Gln	Pro	Ser	Gln	Arg	Thr								
					405										

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Pro	Arg	Arg	Leu	Leu	Leu	Val	Ala	Ala	Cys	Phe	Ser	Leu	Cys
1				5					10					15	
Gly	Pro	Leu	Leu	Ser	Ala	Arg	Thr	Arg	Ala	Arg	Arg	Pro	Glu	Ser	Lys
			20					25					30		
Ala	Thr	Asn	Ala	Thr	Leu	Asp	Pro	Arg	Ser	Phe	Leu	Leu	Arg	Asn	Pro
		35					40					45			
Asn	Asp	Lys	Tyr	Glu	Pro	Phe	Trp	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Ser
	50					55				60					
Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu
65					70				75					80	
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu
			85					90					95		
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val
			100					105					110		
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile
		115					120					125			
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu
	130					135					140				
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser
145				150						155					160
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg
			165						170					175	

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Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu
			180					185					190		
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met
		195					200					205			
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu
	210					215					220				
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys
225					230					235					240
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp
			245						250					255	
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser
			260					265						270	
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val
		275					280					285			
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn
	290					295					300				
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys
305					310						315				320
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His
				325					330					335	
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala
			340					345					350		
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro
		355					360					365			
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser
	370					375					380				
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser
385					390					395					400
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn
			405						410					415	
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr							
		420						425							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Ser	Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu
1				5				10					15		
Ala	Ala	Ser	Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser

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20 25 30
 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
 35 40 45
 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
 50 55 60
 Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
 65 70 75 80
 Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala
 85 90 95
 Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
 100 105 110
 Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
 115 120 125
 Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly
 130 135 140
 Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
 145 150 155 160
 Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
 165 170 175
 Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile
 180 185 190
 Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro
 195 200 205
 Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr
 210 215 220
 Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Pro Phe
 225 230 235 240
 Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala
 245 250 255
 Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp
 260 265 270
 Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr
 275 280 285
 Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu
 290 295 300
 Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr
 305 310 315 320
 Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile
 325 330 335
 Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala
 340 345 350
 Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln
 355 360 365
 Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser
 370 375 380
 Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21,

and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and

27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, an

d 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKBTC

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met	Asp	Ser	Lys	Gly	Ser	Ser	Gln	Lys	Gly	Ser	Arg	Leu	Leu	Leu	Leu
1				5					10					15	
Leu	Val	Val	Ser	Asn	Leu	Leu	Leu	Cys	Gln	Gly	Val	Val	Ser	Asp	Tyr
			20					25					30		
Lys	Asp	Asp	Asp	Asp	Val	Glu									
			35												

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe	Glu	Glu	Phe	Pro
1				5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

El Cont

Leu	Thr	Pro	Lys
1			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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Thr Phe Arg Gly Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
1 5 10 15
Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
1 5 10 15

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Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu
1 5 10 15
Glu Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
1 5 10 15
Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys

1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

1

1